



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/007,747

DATE: 03/20/2002

TIME: 11:52:40

Input Set : N:\Crf3\RULE60\10007747.raw

Output Set: N:\CRF3\03202002\J007747.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Daggett, Lorrie P.

3 Ellis, Steven B.

4 Liaw, Chen W.

5 Lu, Chin-Chun

6 (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

7 SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

8 (iii) NUMBER OF SEQUENCES: 63

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Heller Ehrman White & McAuliffe

11 (B) STREET: 4250 Executive Square, 7th Floor

12 (C) CITY: La Jolla

13 (D) STATE: CA

14 (E) COUNTRY: USA

15 (F) ZIP: 92037

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk

18 (B) COMPUTER: IBM PC compatible

19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

21 (vi) CURRENT APPLICATION DATA:

C--> 22 (A) APPLICATION NUMBER: US/10/007,747

C--> 23 (B) FILING DATE: 07-Dec-2001

24 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: US/09/648,797

26 (B) FILING DATE: 28-Aug-2000

27 (A) APPLICATION NUMBER: US/08/940,086A

28 (B) FILING DATE: 29-SEPT-97

29 (A) APPLICATION NUMBER: US 08/231,193

30 (B) FILING DATE: 20-APR-1994

31 (A) APPLICATION NUMBER: US 08/052,449

32 (B) FILING DATE: 20-APR-1993

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Seidman, Stephanie

35 (B) REGISTRATION NUMBER: 33,779

36 (C) REFERENCE/DOCKET NUMBER: 24735-9383C

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: (619) 450-8400

39 (B) TELEFAX: (619) 450-8499

40 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:

42 (A) LENGTH: 4298 base pairs

ENTERED

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43 (B) TYPE: nucleic acid
44 (C) STRANDEDNESS: both
45 (D) TOPOLOGY: both
46 (ii) MOLECULE TYPE: cDNA
47 (ix) FEATURE:
48 (A) NAME/KEY: CDS
49 (B) LOCATION: 262..3078
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51 CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG 60
52 CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC 120
53 CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGACGCC CGCGGGGCCG GGCGAGCGCA 180
54 GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG 240
55 CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC 291
56 Met Ser Thr Met Arg Leu Leu Thr Leu Ala
57 1 5 10
58 CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC 339
59 Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile
60 15 20 25
61 GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC 387
62 Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe
63 30 35 40
64 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT 435
65 Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile
66 45 50 55
67 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG 483
68 Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met
69 60 65 70
70 GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC 531
71 Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile
72 75 80 85 90
73 CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT 579
74 Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro
75 95 100 105
76 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC 627
77 Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr
78 110 115 120
79 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG 675
80 Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu
81 125 130 135
82 CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG 723
83 Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met
84 140 145 150
85 ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC 771
86 Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp
87 155 160 165 170
88 CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG 819
89 His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu
90 175 180 185
91 CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG 867

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Input Set : N:\Crf3\RULE60\10007747.raw

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| | | |
|-----|---|------|
| 92 | Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys | |
| 93 | 190 195 200 | |
| 94 | AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC | 915 |
| 95 | Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val | |
| 96 | 205 210 215 | |
| 97 | ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA | 963 |
| 98 | Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala | |
| 99 | 220 225 230 | |
| 100 | GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC | 1011 |
| 101 | Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly | |
| 102 | 235 240 245 250 | |
| 103 | GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC | 1059 |
| 104 | Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile | |
| 105 | 255 260 265 | |
| 106 | CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC | 1107 |
| 107 | Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser | |
| 108 | 270 275 280 | |
| 109 | GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG | 1155 |
| 110 | Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys | |
| 111 | 285 290 295 | |
| 112 | GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC | 1203 |
| 113 | Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile | |
| 114 | 300 305 310 | |
| 115 | TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT | 1251 |
| 116 | Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr | |
| 117 | 315 320 325 330 | |
| 118 | GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG | 1299 |
| 119 | Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg | |
| 120 | 335 340 345 | |
| 121 | AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG | 1347 |
| 122 | Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val | |
| 123 | 350 355 360 | |
| 124 | CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG | 1395 |
| 125 | Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys | |
| 126 | 365 370 375 | |
| 127 | ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG | 1443 |
| 128 | Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met | |
| 129 | 380 385 390 | |
| 130 | TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC | 1491 |
| 131 | Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr | |
| 132 | 395 400 405 410 | |
| 133 | GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC | 1539 |
| 134 | Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val | |
| 135 | 415 420 425 | |
| 136 | AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG | 1587 |
| 137 | Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr | |
| 138 | 430 435 440 | |
| 139 | TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT | 1635 |
| 140 | Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe | |

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| | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|
| 141 | | | | 445 | | | | 450 | | | | 455 | | | | | | | | |
| 142 | TGC | ATC | GAC | CTG | CTC | ATC | AAG | CTG | GCA | CGG | ACC | ATG | AAC | TTC | ACC | TAC | 1683 | | | |
| 143 | Cys | Ile | Asp | Leu | Leu | Ile | Lys | Leu | Ala | Arg | Thr | Met | Asn | Phe | Thr | Tyr | | | | |
| 144 | 460 | | | | | | | 465 | | | 470 | | | | | | | | | |
| 145 | GAG | GTG | CAC | CTG | GTG | GCA | GAT | GGC | AAG | TTC | GGC | ACA | CAG | GAG | CGG | GTG | 1731 | | | |
| 146 | Glu | Val | His | Leu | Val | Ala | Asp | Gly | Lys | Phe | Gly | Thr | Gln | Glu | Arg | Val | | | | |
| 147 | 475 | | | | | | | 480 | | | 485 | | | | 490 | | | | | |
| 148 | AAC | AAC | AGC | AAC | AAG | AAG | GAG | TGG | AAT | GGG | ATG | ATG | GGC | GAG | CTG | CTC | 1779 | | | |
| 149 | Asn | Asn | Ser | Asn | Lys | Lys | Glu | Trp | Asn | Gly | Met | Met | Gly | Glu | Leu | Leu | | | | |
| 150 | | | | 495 | | | | 500 | | | | | | | 505 | | | | | |
| 151 | AGC | GGG | CAG | GCA | GAC | ATG | ATC | GTG | GCG | CCG | CTA | ACC | ATA | AAC | AAC | GAG | 1827 | | | |
| 152 | Ser | Gly | Gln | Ala | Asp | Met | Ile | Val | Ala | Pro | Leu | Thr | Ile | Asn | Asn | Glu | | | | |
| 153 | | | | 510 | | | | 515 | | | | | | | 520 | | | | | |
| 154 | CGC | GCG | CAG | TAC | ATC | GAG | TTT | TCC | AAG | CCC | TTC | AAG | TAC | CAG | GGC | CTG | 1875 | | | |
| 155 | Arg | Ala | Gln | Tyr | Ile | Glu | Phe | Ser | Lys | Pro | Phe | Lys | Tyr | Gln | Gly | Leu | | | | |
| 156 | 525 | | | | | | | 530 | | | | | | | 535 | | | | | |
| 157 | ACT | ATT | CTG | GTC | AAG | AAG | GAG | ATT | CCC | CGG | AGC | ACG | CTG | GAC | TCG | TTC | 1923 | | | |
| 158 | Thr | Ile | Leu | Val | Lys | Lys | Glu | Ile | Pro | Arg | Ser | Thr | Leu | Asp | Ser | Phe | | | | |
| 159 | 540 | | | | | | | 545 | | | | | | | 550 | | | | | |
| 160 | ATG | CAG | CCG | TTC | CAG | AGC | ACA | CTG | TGG | CTG | CTG | GTG | GGG | CTG | TCG | GTG | 1971 | | | |
| 161 | Met | Gln | Pro | Phe | Gln | Ser | Thr | Leu | Trp | Leu | Leu | Val | Gly | Leu | Ser | Val | | | | |
| 162 | 555 | | | | | | | 560 | | | | | | | 565 | | | | | |
| 163 | CAC | GTG | GTG | GCC | GTG | ATG | CTG | TAC | CTG | CTG | GAC | CGC | TTC | AGC | CCC | TTC | 2019 | | | |
| 164 | His | Val | Val | Ala | Val | Met | Leu | Tyr | Leu | Leu | Asp | Arg | Phe | Ser | Pro | Phe | | | | |
| 165 | | | | 575 | | | | 580 | | | | | | | 585 | | | | | |
| 166 | GGC | CGG | TTC | AAG | GTG | AAC | AGC | GAG | GAG | GAG | GAG | GAG | GAC | GCA | CTG | ACC | 2067 | | | |
| 167 | Gly | Arg | Phe | Lys | Val | Asn | Ser | Glu | Glu | Glu | Glu | Glu | Asp | Ala | Leu | Thr | | | | |
| 168 | 590 | | | | | | | 595 | | | | | | | 600 | | | | | |
| 169 | CTG | TCC | TCG | GCC | ATG | TGG | TTC | TCC | TGG | GGC | GTC | CTG | CTC | AAC | TCC | GGC | 2115 | | | |
| 170 | Leu | Ser | Ser | Ala | Met | Trp | Phe | Ser | Trp | Gly | Val | Leu | Leu | Asn | Ser | Gly | | | | |
| 171 | 605 | | | | | | | 610 | | | | | | | 615 | | | | | |
| 172 | ATC | GGG | GAA | GGC | GCC | CCC | AGA | AGC | TTC | TCA | GCG | CGC | ATC | CTG | GGC | ATG | 2163 | | | |
| 173 | Ile | Gly | Glu | Gly | Ala | Pro | Arg | Ser | Phe | Ser | Ala | Arg | Ile | Leu | Gly | Met | | | | |
| 174 | 620 | | | | | | | 625 | | | | | | | 630 | | | | | |
| 175 | GTG | TGG | GCC | GGC | TTT | GCC | ATG | ATC | ATC | GTG | GCC | TCC | TAC | ACC | GCC | AAC | 2211 | | | |
| 176 | Val | Trp | Ala | Gly | Phe | Ala | Met | Ile | Ile | Val | Ala | Ser | Tyr | Thr | Ala | Asn | | | | |
| 177 | 635 | | | | | | | 640 | | | | | | | 645 | | | | | |
| 178 | CTG | GCG | GCC | TTC | CTG | GTG | CTG | GAC | CGG | CCG | GAG | GAG | CGC | ATC | ACG | GGC | 2259 | | | |
| 179 | Leu | Ala | Ala | Phe | Leu | Val | Leu | Asp | Arg | Pro | Glu | Glu | Arg | Ile | Thr | Gly | | | | |
| 180 | | | | 655 | | | | 660 | | | | | | | 665 | | | | | |
| 181 | ATC | AAC | GAC | CCT | CGG | CTG | AGG | AAC | CCC | TC | | | | | | | | | | |

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| | | |
|-----|--|------|
| 190 | GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC | 2451 |
| 191 | Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile | |
| 192 | 715 720 725 730 | |
| 193 | TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG | 2499 |
| 194 | Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu | |
| 195 | 735 740 745 | |
| 196 | GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG | 2547 |
| 197 | Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met | |
| 198 | 750 755 760 | |
| 199 | CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG | 2595 |
| 200 | Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys | |
| 201 | 765 770 775 | |
| 202 | TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG | 2643 |
| 203 | Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg | |
| 204 | 780 785 790 | |
| 205 | TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT | 2691 |
| 206 | Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe | |
| 207 | 795 800 805 810 | |
| 208 | GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC | 2739 |
| 209 | Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala | |
| 210 | 815 820 825 | |
| 211 | GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT | 2787 |
| 212 | Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp | |
| 213 | 830 835 840 | |
| 214 | GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG | 2835 |
| 215 | Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp | |
| 216 | 845 850 855 | |
| 217 | CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT | 2883 |
| 218 | Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro | |
| 219 | 860 865 870 | |
| 220 | AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC | 2931 |
| 221 | Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser | |
| 222 | 875 880 885 890 | |
| 223 | TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC | 2979 |
| 224 | Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg | |
| 225 | 895 900 905 | |
| 226 | GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT | 3027 |
| 227 | Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile | |
| 228 | 910 915 920 | |
| 229 | GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC | 3075 |
| 230 | Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser | |
| 231 | 925 930 935 | |
| 232 | TGAGACTCCC CGCCCGCCCT CCTCTGCCCC CTCCCCGCA GACAGACAGA CAGACGGACG | 3135 |
| 233 | GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC | 3195 |
| 234 | CCAGCTCCC CCAGGTGCG CCTGCCC GCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC | 3255 |
| 235 | GTCCCGGCC CGCGGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGCTCT GTGTATTCT | 3315 |
| 236 | ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTTCG | 3375 |
| 237 | GTCAGCACCG TGGTGTGAGG CCCCCGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG | 3435 |
| 238 | ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG | 3495 |

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 18
Seq#:47; N Pos. 18
Seq#:49; N Pos. 18
Seq#:51; N Pos. 18
Seq#:53; N Pos. 18
Seq#:57; Xaa Pos.1147,1171
Seq#:58; Xaa Pos.1147,1171

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1493 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1499 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1508 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1511 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1517 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1520 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1529 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1535 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
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L:2813 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2816 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2819 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
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L:2825 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2828 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2834 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2837 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2840 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
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L:2855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2861 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2864 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
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L:2873 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2876 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2885 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25

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DATE: 03/20/2002

TIME: 11:52:41

Input Set : N:\Crf3\RULE60\10007747.raw

Output Set: N:\CRF3\03202002\J007747.raw

L:3058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:9138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:3937
L:9144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:4033
L:9330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1136
L:9334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1168